

AMENDMENTS TO THE SPECIFICATION

Please replace Paragraph [0069] with the following paragraph rewritten in amendment format:

[0069] Identification of orthologs may also be performed. In various configurations of the disclosed methods and referring to Figure 2, human-mouse orthologs can be identified at step 114 utilizing two runs of tBlastX between the Celera human and mouse transcripts (for Blast definitions, see, for example, <http://www.ncbi.nlm.nih.gov/BLAST>). An E value cut-off of $< 10^{-4}$ may be used, with subject 110 and query 112 databases swapped between runs. Next, mutually best transcript pairs can be selected at step 116 as putative orthologs between the two species. Mutually best hits can be the top hits in both runs of tBlastX. The same approach can be used to identify orthologs in more than two species.

Please replace Paragraph [00137] with the following paragraph rewritten in amendment format:

[00137] The viewer software may be invoked and used in various ways. Various configurations of a synteny viewer may be provided as software stored on a user's computer system, such as a personal computer and display. Although various types of personal computers can be available that run a variety of operating systems, the invocation and use of configurations of the viewer will be described in connection with the Microsoft® Windows® MICROSOFT® WINDOWS® operating system. Any modifications that may be necessary for invocation and use of configurations of synteny viewers for other computer operating systems, such as the OS/X® operating system for Apple® Computer systems and the Linux® operating system, among others, will be

readily apparent to those having ordinary skill in the art for coding programs in such operating systems upon reading the description contained herein.